cont A1

a) providing nucleic acid molecules that are (i) target nucleic acid molecules in said sample, or (ii) probes that hybridize to target nucleic acid molecules in said sample, or (iii) amplification products of (i) or (ii), or (iv) a genomic representation of (i); and

b) detecting target nucleic acid molecules by contacting or comparing the nucleic acid molecules of (a) with a detection ensemble of nucleic acid sequences that has a minimum genomic derivation of greater than five and that comprises nucleic acid detection sequences that can detect [target nucleic acid molecules] the nucleic acid molecules of (a).

A2

4. (Amended) The method of claim 1, wherein size fractionated fragments of the nucleic acid molecules of step (a) are not immobilized [as size fractionated fragments] in a matrix or on a solid support.

5. (Amended) The method of claim [1,] 8, further comprising using [fewer than four pairs of] amplification sequences to amplify the probes of step (a) (ii), to yield, if target nucleic acid molecules are present in the sample, [amplification products.] amplified probes.

A3

7. (Amended) The method of claim 1, wherein said method is used to quantify a target organism in said biological sample by *in situ* hybridization following step (b).

8. (Amended) The method of claim 1, wherein prior to step (a), nucleic acid molecules of said sample are hybridized, simultaneously, with an ensemble of ID probes or SNP probes to yield the probes of step (a)(ii).

A4

11. (Amended) The method of claim 1, wherein the physical state of said nucleic acid molecules of step (a) [are in] is the liquid phase.

15. (Amended) The method of claim 8, wherein said ensemble of ID probes

A5

includes probes that hybridize to at least two different regions of the genome [nucleic acid molecules from each] of at least ten different viruses, each of which belongs to a different genus.

16. (Amended) The method of claim 1, wherein said biological sample is a gastrointestinal tract sample and [said genetic information is the identification of nucleic acid molecules] wherein said target nucleic acid molecules in said sample [from] comprise 6 or more different nucleic acid molecules from [of] *Escherichia coli,* Salmonella, Shigella, *Yersinia enterocolitica, Vibrio cholera, Campylobacter fecalis, Clostridium difficile,* Rotavirus, Norwalk virus, Astrovirus, Adenovirus, Coronavirus, *Giardia lamblia, Entamoeba histolytica, Blastocystis hominis,* Cryptosporidium, Microsporidium, *Enterobius vermicularis, Strongyloides stercoralis, Opsthorchis viverrini, Clonorchis sinensis,* and *Hymenoplepis nana.*

17. (Amended) The method of claim 1, wherein said biological sample is a respiratory tract sample, and [said genetic information is the identification of nucleic acid molecules] wherein said target nucleic acid molecules in said sample [from] comprise 6 or more different nucleic acid molecules from [of] *Cornybacterium diphtheriae, Mycobacterium tuberculosis, Mycoplasma pneumoniae, Chlamydia trachomatis, Chlamydia pneumoniae, Bordetella pertussis,* Legionella spp., Nocardia spp.,

Pseudomonas aeruginosa, Staphylococcus aureus, Histoplasma capsulatum, Coccidoides immitis, Cryptococcus neoformans, Blastomyces dermatitidis, Pneumocystis carinii, Respiratory Syncytial Virus, Adenovirus, Herpes simplex virus, Influenza virus, Parainfluenza virus, and Rhinovirus.

18. (Amended) The method of claim 1, wherein said biological sample is a blood tract sample, and [said genetic information is the identification of nucleic acid molecules] wherein said target nucleic acid molecules in said sample [from] comprise 6 or more different nucleic acid molecules from [of] Coagulase-negative *staphylococci, Staphylococcus aureus, Viridans streptococci,* Enterococcus spp., Beta-hemolytic streptococci, *Streptococcus pneumoniae,* Escherichia spp., Klebsiella spp., Pseudomonas spp., Enterbater spp., Proteus spp., Bacteroides spp., Clostridium spp., *Pseudomonas aueruginosa,* Cornybacterium spp., Plasmodium spp., *Leishmania donovani,* Toxoplasma spp., Microfilariae, Fungi, *Histoplasma capsulatum, Coccidoides immitis, Cryptococcus neoformans,* Candida spp., HIV, Herpes simplex virus, Hepatitis C virus, Hepatitis B virus, Cytomegalovirus, and Epstein-Barr virus.

19. (Amended) The method of claim 1, [wherein said genetic information is the identification of nucleic acid molecules] wherein said target nucleic acid molecules in said sample [from] comprise 6 or more different nucleic acid molecules from [of] coxsakievirus A, Herpes simplex virus, St. Louis encephalitis virus, Epstein-Barr virus, myxovirus, JC virus, coxsakievirus B, togavirus, measles virus, a hepatitis virus, paramyxovirus, echovirus, bunyavirus, cytomegalovirus, varicella-zoster virus, HIV

mumps virus, equine encephalitis virus, lymphocytic choriomeningitis virus, rabies virus, and BK virus.

cont A5

20. (Amended) The method of claim 8, wherein at least 50% of the probes comprising said ensemble of ID [nucleic acid] probes are capable of hybridizing to pre-determined genomic difference sequences that are potentially present in said sample or in a genomic representation of said sample.

A6

47. (Amended) A method for [obtaining genetic information from] detecting and identifying target nucleic acid molecules in a biological sample potentially comprising target nucleic acid molecules, said method comprising the steps of:

a) providing an ensemble of nucleic acid probes having a minimum genomic derivation of greater than five;

b) contacting said ensemble of probes, simultaneously, with nucleic acid molecules of said sample;

Add new claims 58, 59, and 60:

--58. The method of claim 5, wherein said amplification is carried out using fewer than four pairs of amplification sequences.

A7

59. The method of claim 5, wherein said biological sample is treated to make nucleic molecules available for hybridization without purifying said nucleic acid molecules from said sample.